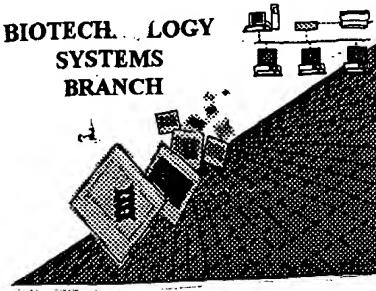


0590  
0806

BIOTECH. LOGY  
SYSTEMS  
BRANCH



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/721,904  
Source: OPE  
Date Processed by STIC: 8/7/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be downloaded from the USPTO website at the following address:**  
**<http://www.uspto.gov/web/offices/pac/checker>**

**Raw Sequence Listing Error Summary**

<b>ERROR DETECTED</b>	<b>SUGGESTED CORRECTION</b>	<b>SERIAL NUMBER: <u>09/721,904</u></b>
<b>ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHIA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE</b>		
1 <input type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped	
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/721,904

DATE: 08/07/2001  
TIME: 13:33:47

Input Set : A:\seqlist.asc.txt  
Output Set: N:\CRF3\08072001\I721904.raw

Does Not Comply  
Corrected Diskette Needed

3 <110> APPLICANT: JULIUS, Michael H.  
4 FILIPP, Dominik  
6 <120> TITLE OF INVENTION: THE INDUCTION OF ANTIBIOTIC PROTEINS AND PEPTIDES BY  
7 LAIT/sCD14-PROTEIN  
9 <130> FILE REFERENCE: 47841/00063  
11 <140> CURRENT APPLICATION NUMBER: US 09/721,904  
12 <141> CURRENT FILING DATE: 2000-11-27  
14 <150> PRIOR APPLICATION NUMBER: PCT/CA99/00482  
15 <151> PRIOR FILING DATE: 1999-05-27  
17 <150> PRIOR APPLICATION NUMBER: US 60/086,884  
18 <151> PRIOR FILING DATE: 1998-05-27  
20 <160> NUMBER OF SEQ ID NOS: 8  
22 <170> SOFTWARE: Wordperfect 9.0

MP2 1-3

## ERRORED SEQUENCES

159 <210> SEQ ID NO: 4  
160 <211> LENGTH: 3738 (p.2)  
161 <212> TYPE: PRY  
162 <213> ORGANISM: bovine  
164 <400> SEQUENCE: 4  
165 Met Val Cys Val Pro Tyr Leu Leu Leu Leu Leu Pro Ser Leu Leu  
166 1 5 10 15  
168 Arg Val Ser Ala Asp Thr Thr Glu Pro Cys Glu Leu Asp Asp Asp Asp  
169 20 25 30  
171 Phe Arg Cys Val Cys Asn Phe Thr Asp Pro Lys Pro Asp Trp Ser Ser  
172 35 40 45  
174 Ala Val Gln Cys Met Val Ala Val Glu Val Glu Ile Ser Ala Gly Gly  
175 50 55 60  
177 Arg Ser Leu Glu Gln Phe Leu Lys Gly Ala Asp Thr Asn Pro Lys Gln  
178 65 70 75 80  
180 Tyr Ala Asp Thr Ile Lys Ala Leu Arg Val Arg Arg Leu Lys Leu Gly  
181 85 90 95  
183 Ala Ala Gln Val Pro Ala Gln Leu Leu Val Ala Val Leu Arg Ala Leu  
184 100 105 110  
186 Gly Tyr Ser Arg Leu Lys Glu Leu Thr Leu Glu Asp Leu Glu Val Thr  
187 115 120 125  
189 Gly Pro Thr Pro Pro Thr Pro Leu Glu Ala Ala Gly Pro Ala Leu Thr  
190 130 135 140  
192 Thr Leu Ser Leu Arg Asn Val Ser Trp Thr Thr Gly Gly Ala Trp Leu  
193 145 150 155 160  
195 Gly Glu Leu Gln Gln Trp Leu Lys Pro Gly Leu Arg Val Leu Asn Ile  
196 165 170 175  
198 Ala Gln Ala His Ser Leu Ala Phe Pro Cys Ala Gly Leu Ser Thr Phe  
199 180 185 190  
201 Glu Ala Leu Thr Thr Leu Asp Leu Ser Asp Asn Pro Ser Leu Gly Asp

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/721,904

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Input Set : A:\seqlist.asc.txt  
Output Set: N:\CRF3\08072001\I721904.raw

202	195	200	205
204	Thr Gly Leu Met Ala Ala Leu Cys Pro Asn Lys Phe Pro Ala Leu Gln		
205	210	215	220
207	Tyr Leu Ala Leu Arg Asn Ala Gly Met Glu Thr Pro Ser Gly Val Cys		
208	225	230	235
210	Ala Ala Leu Ala Ala Arg Val Gln Pro Gln Ser Leu Asp Leu Ser		240
211	245	250	255
213	His Asn Ser Leu Arg Val Thr Ala Pro Gly Ala Thr Arg Cys Val Trp		
214	260	265	270
216	Pro Ser Ala Leu Arg Ser Leu Asn Leu Ser Phe Ala Gly Leu Glu Gln		
217	275	280	285
219	Val Pro Lys Gly Leu Pro Pro Lys Leu Ser Val Leu Asp Leu Ser Cys		
220	290	295	300
222	Asn Lys Leu Ser Arg Glu Pro Arg Arg Asp Glu Leu Pro Glu Val Asn		
223	305	310	315
225	Asp Leu Thr Leu Asp Gly Asn Pro Phe Leu Asp Pro Gly Ala Leu Gln		320
226	325	330	335
228	His Gln Asn Asp Pro Met Ile Ser Gly Val Val Pro Ala Cys Ala Arg		
229	340	345	350
231	Ser Ala Leu Thr Met Gly Val Ser Gly Ala Leu Ala Leu Leu Gln Gly		
232	355	360	365
234	Ala Arg Gly Phe Ala		
<b>E--&gt;</b>	<b>235</b>	<b>370</b>	
393	<210> SEQ ID NO: 7		
394	<211> LENGTH: 377		
395	<212> TYPE: PRT		
396	<213> ORGANISM: rabbit		
398	<400> SEQUENCE: 7		
<b>E--&gt;</b>	<b>399</b>	<b>Met Glu Pro Val Pro Cys Leu Leu Leu Leu Leu Pro Xaa Leu Leu</b>	
400	1	5	10
402	Arg Ala Ser Thr Asp Thr Pro Glu Pro Cys Glu Leu Asp Asp Asp Asp		
403	20	25	30
405	Ile Arg Cys Val Cys Asn Phe Ser Asp Pro Gln Pro Asp Trp Ser Ser		
406	35	40	45
408	Ala Leu Gln Cys Met Pro Ala Val Gln Val Glu Met Trp Gly Gly Gly		
409	50	55	60
411	His Ser Leu Glu Gln Phe Leu Arg Gln Ala Asp Leu Tyr Thr Asp Gln		
412	65	70	75
414	Arg Arg Tyr Ala Asp Val Val Lys Ala Leu Arg Val Arg Arg Leu Thr		80
415	85	90	95
417	Val Gly Ala Val Gln Val Pro Ala Pro Leu Leu Leu Gly Val Leu Arg		
418	100	105	110
420	Val Leu Gly Tyr Ser Arg Leu Lys Glu Leu Ala Leu Glu Asp Ile Glu		
421	115	120	125
423	Val Thr Gly Thr Ala Pro Pro Pro Pro Leu Glu Ala Thr Gly Pro		
424	130	135	140
426	Ala Leu Ser Thr Leu Ser Leu Arg Asn Val Ser Trp Pro Lys Gly Gly		
427	145	150	155
429	Ala Trp Leu Ser Glu Leu Gln Gln Trp Leu Lys Pro Gly Leu Gln Val		160

all item 9 on  
Error  
summary  
sheet

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/721,904

DATE: 08/07/2001  
TIME: 13:33:47

Input Set : A:\seqlist.asc.txt  
Output Set: N:\CRF3\08072001\I721904.raw

430 165 170 175  
432 Leu Asn Ile Ala Gln Ala His Thr Leu Ala Phe Ser Cys Glu Gln Val  
433 180 185 190  
435 Arg Thr Phe Ser Ala Leu Thr Thr Leu Asp Leu Ser Glu Asn Pro Gly  
436 195 200 205  
438 Leu Gly Glu Arg Gly Leu Val Ala Ala Leu Cys Pro His Lys Glu Pro  
439 210 215 220  
441 Ala Leu Gln Asp Leu Ala Leu Arg Asn Ala Gly Met Lys Ile Leu Gln  
442 225 230 235 240  
444 Gly Val Cys Ala Ala Leu Ala Glu Ala Gly Val Gln Pro His His Leu  
445 245 250 255  
E--> 447 Asp Leu Ser His Asn Ser Leu Arg (Xaa Xaa Xaa) Ala (Xaa) Asp Thr Gln  
448 260 265 270  
450 Arg Cys Ile Trp Pro Ser Ala Leu Asn Ser Leu Asn Leu Ser Phe Thr  
451 275 280 285  
453 Gly Leu Gln Gln Val Pro Lys Gly Leu Pro Ala Lys Leu Asn Val Leu  
454 290 295 300  
456 Asp Leu Ser Cys Asn Lys Leu Asn Arg Ala Pro Gln Pro Gly Glu Leu  
457 305 310 315 320  
459 Pro Lys Val Val Asn Leu Ser Leu Asp Gly Asn Pro Phe Leu Val Pro  
460 325 330 335  
462 Gly Ala Ser Lys Leu Gln Glu Asp Leu Thr Asn Ser Gly Val Phe Pro  
463 340 345 350  
465 Ala Cys Pro Pro Ser Pro Leu Ala Met Gly Met Ser Gly Thr Leu Ala  
466 355 360 365  
468 Leu Leu Gln Gly Ala Arg Gly Phe Ile  
469 370 375

Line 9

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/721,904

DATE: 08/07/2001  
TIME: 13:33:48

Input Set : A:\seqlist.asc.txt  
Output Set: N:\CRF3\08072001\I721904.raw

L:120 M:112 C: (48) String data converted to lower case,  
M:112 Repeated in SeqNo=3  
L:235 M:252 E: No. of Seq. differs, <211>LENGTH:Input:3738 Found:373 SEQ:4  
L:399 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:7  
M:340 Repeated in SeqNo=7